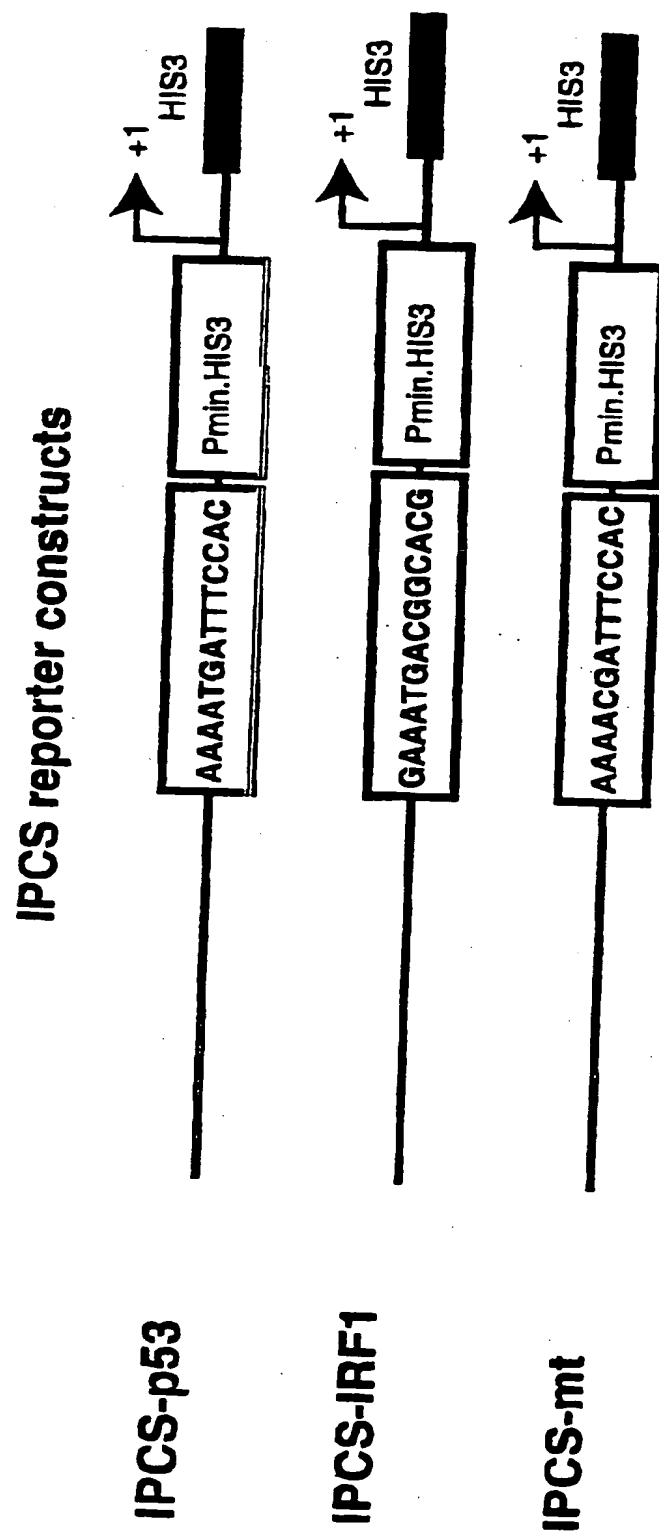
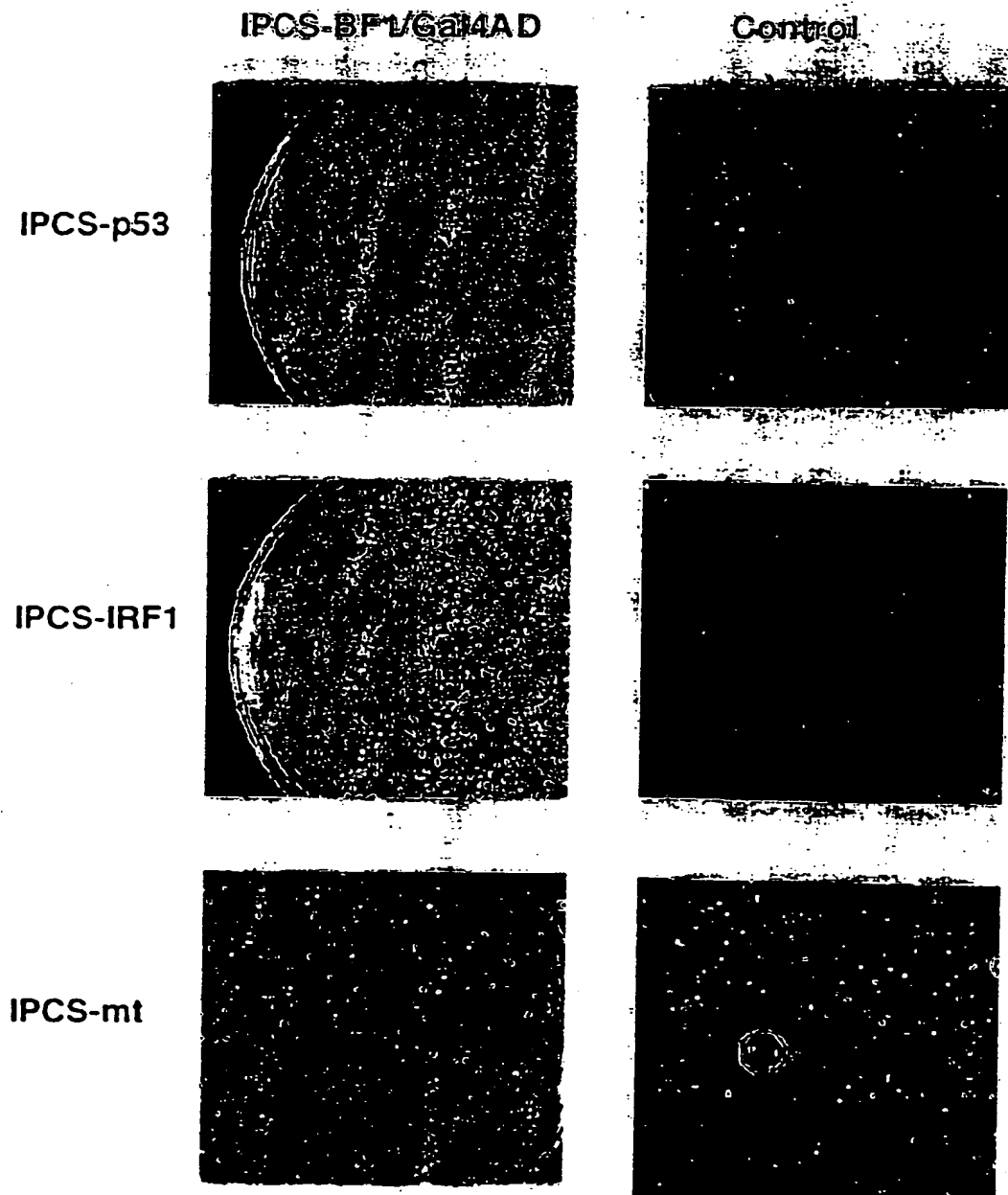


Figure 1A



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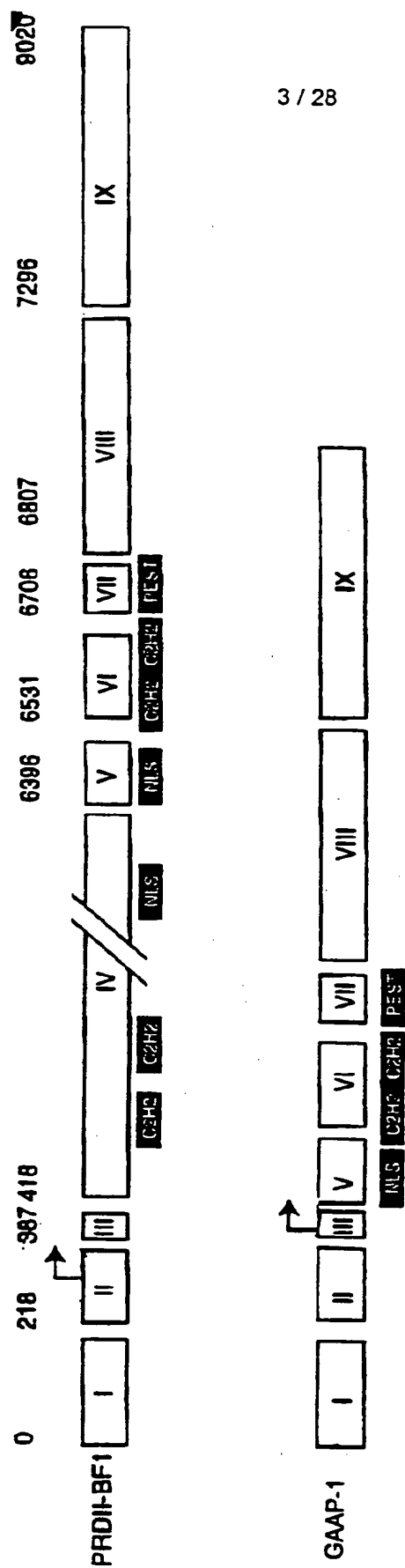
Figure 1B



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Figure 2A

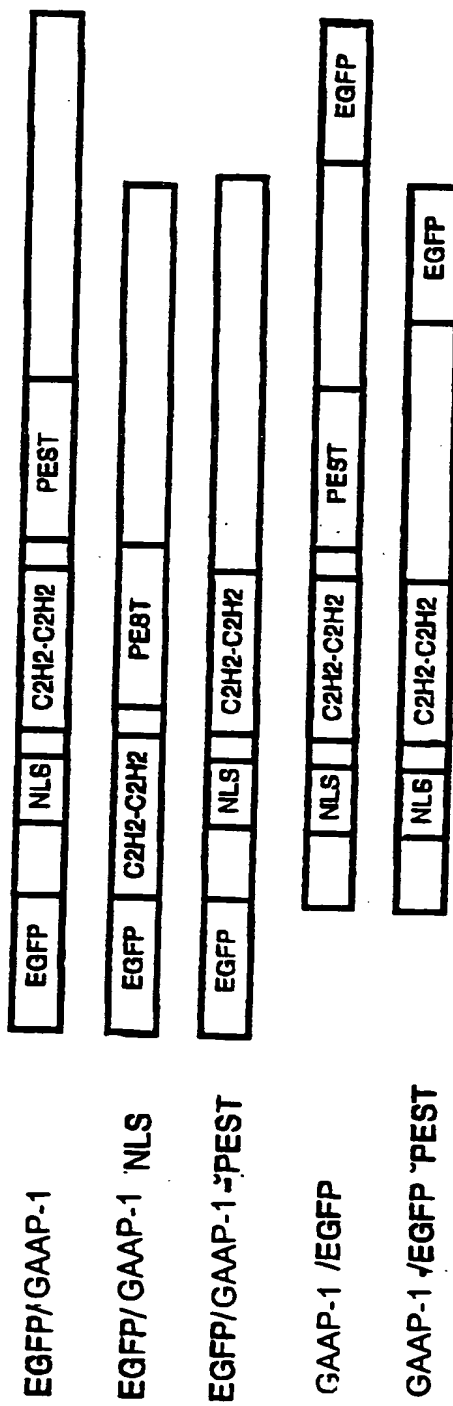


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Figure 3

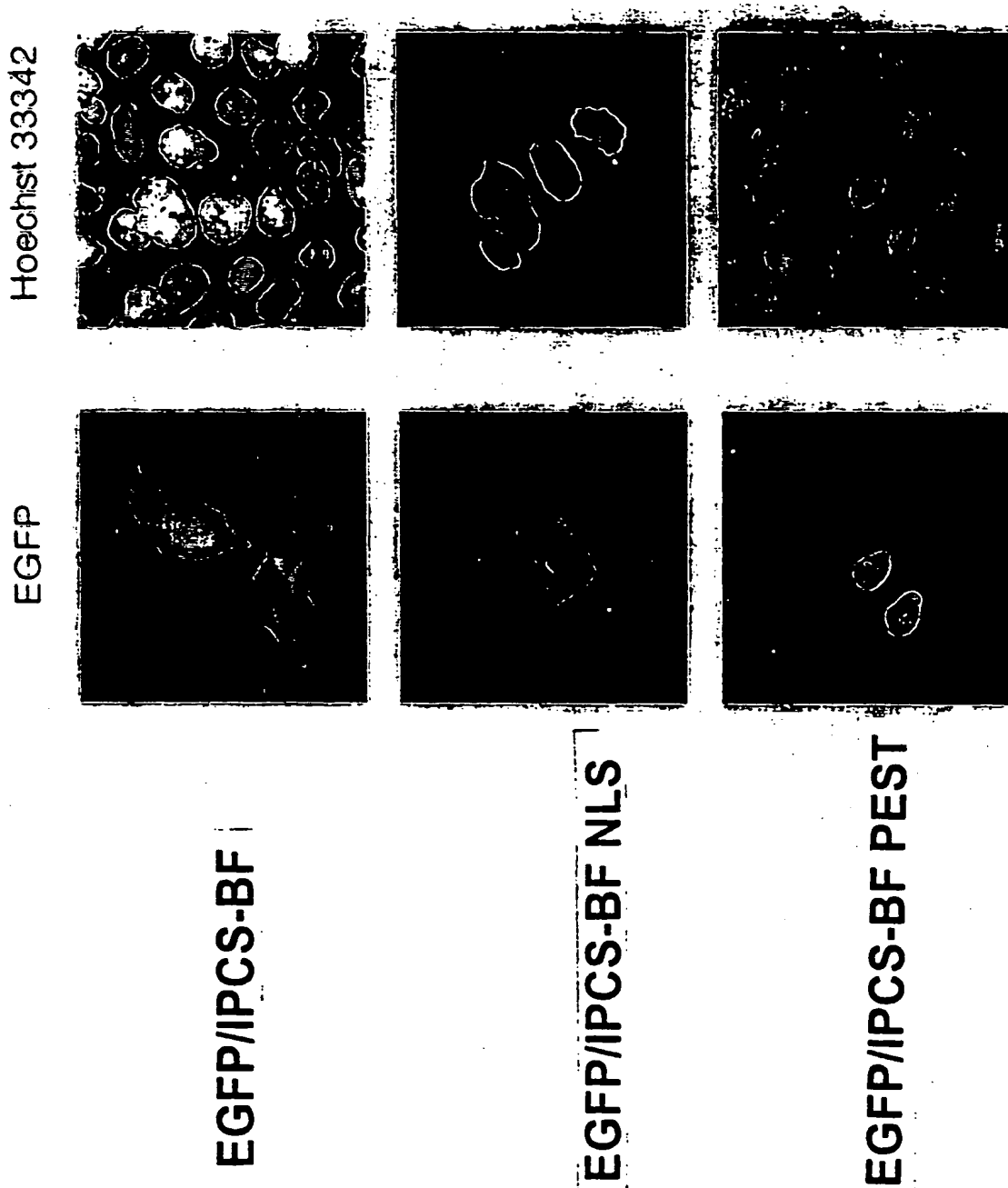
AA 1 M A L G N Q K S T W E F S N K D A S E I N S E Q D K E N S L I **NLS** K S E P H R I K I F
 51 D G G Y K S N E E Y V Y I R G R G R G K **CR12** V I C E E C G I R C K K P S M I K K H I R T H T D V R P Y H
 61 I C T Y C N E S E F K T K G N L T K H M K S K A H S K K C V D L G I S V G L I D E Q D T E E S D E K Q R
 151 F S Y E R S G Y D L E E S D G P D E D D N E N E D D D E D S Q A E S V L S A T P S V T A S P Q H L P
 201 S R S S L Q D P V S T D E D V R I T D C F S G V H T D P M D V L P R A L T R M T V L S T A Q S D Y
 251 N R K T L S P G K A R Q R A A R D E N D T I P S V D T S R S P C H Q M S V D Y P E S E E I L R S S M
 301 A G K A V A I T Q S P S S V R L P P A A A E H S P Q T A A G M P S V A S P H P D P Q E Q K Q Q I T L
 351 Q P T P G L P S P H T H L F S H L P L H S Q Q Q S R T P Y N M V P V G G I H V V P A G L T Y S T F V
 401 P L Q A G P V Q L T I P A V S W H R T L G T H R N T V T E V S G T T N P A G V A E L S S V V P C I
 451 P I G Q I R V P G L Q N L S T P G L Q S L P S L S M E T V N I V G L A N T N M A P Q V H P P G L A L
 501 N A V G L Q V L T A N P S S Q S S P A P Q A H I P G L Q I L N I A L P T L I P S V S Q V A V D A Q G
 551 A P E M P A S Q S K A C E T Q P K Q T S V A S A N Q V S R T E S P Q G L P T V Q R E N A K K V L N P
 601 P A P A G D H A R L D G L S K M D T E K A A S A N H V K P K P E L T S I Q G Q P A S T S Q P L L K A
 651 H S E V F T K P S G Q Q T L S P D R Q V P R P T G L P R R Q P T V H F S D V S S D D E D R L V I A
 701 T

Figure 4A



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Figure 4B



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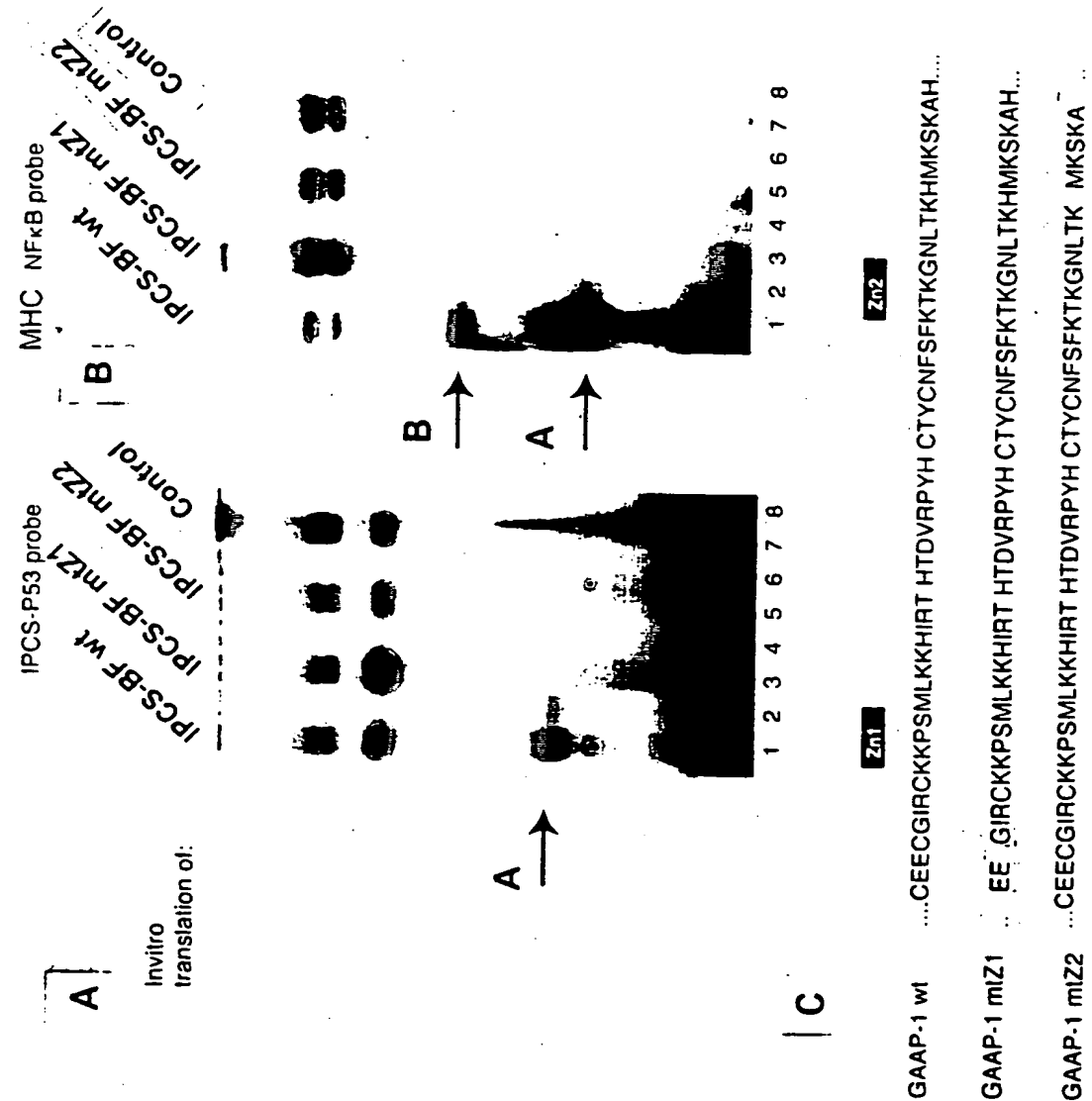
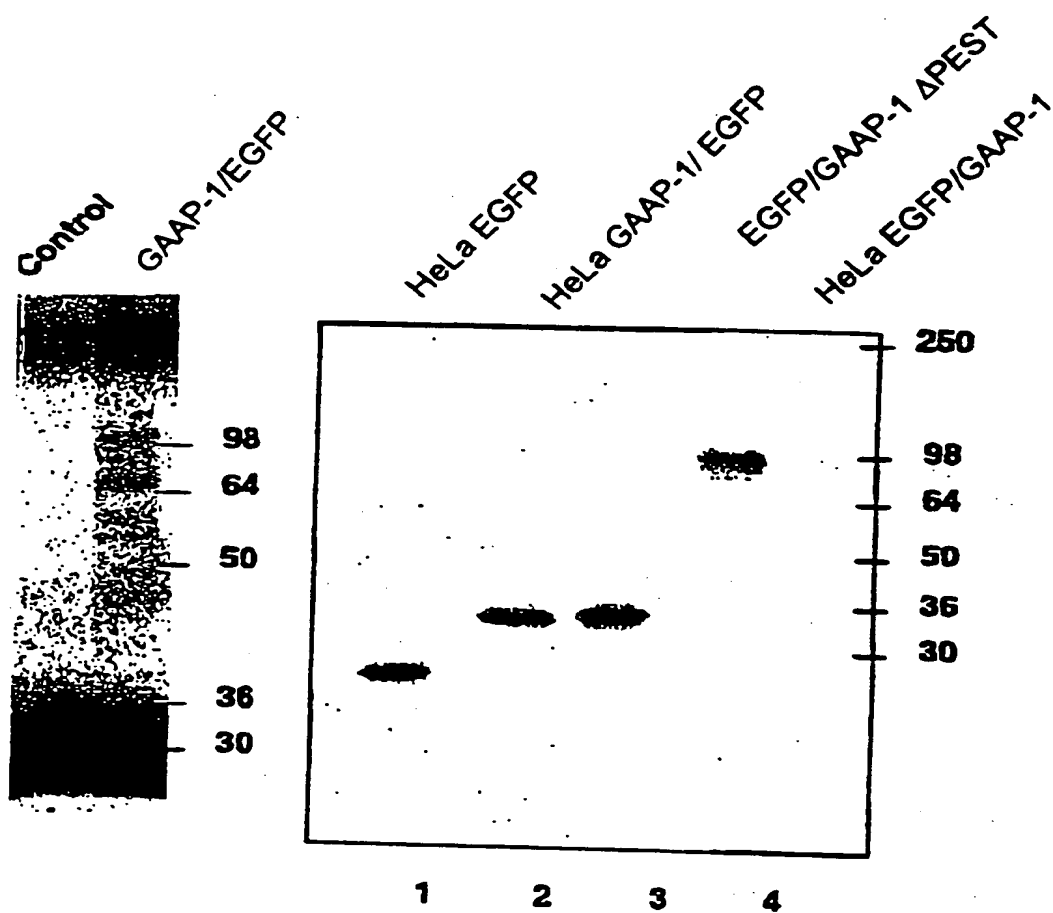


Figure 6

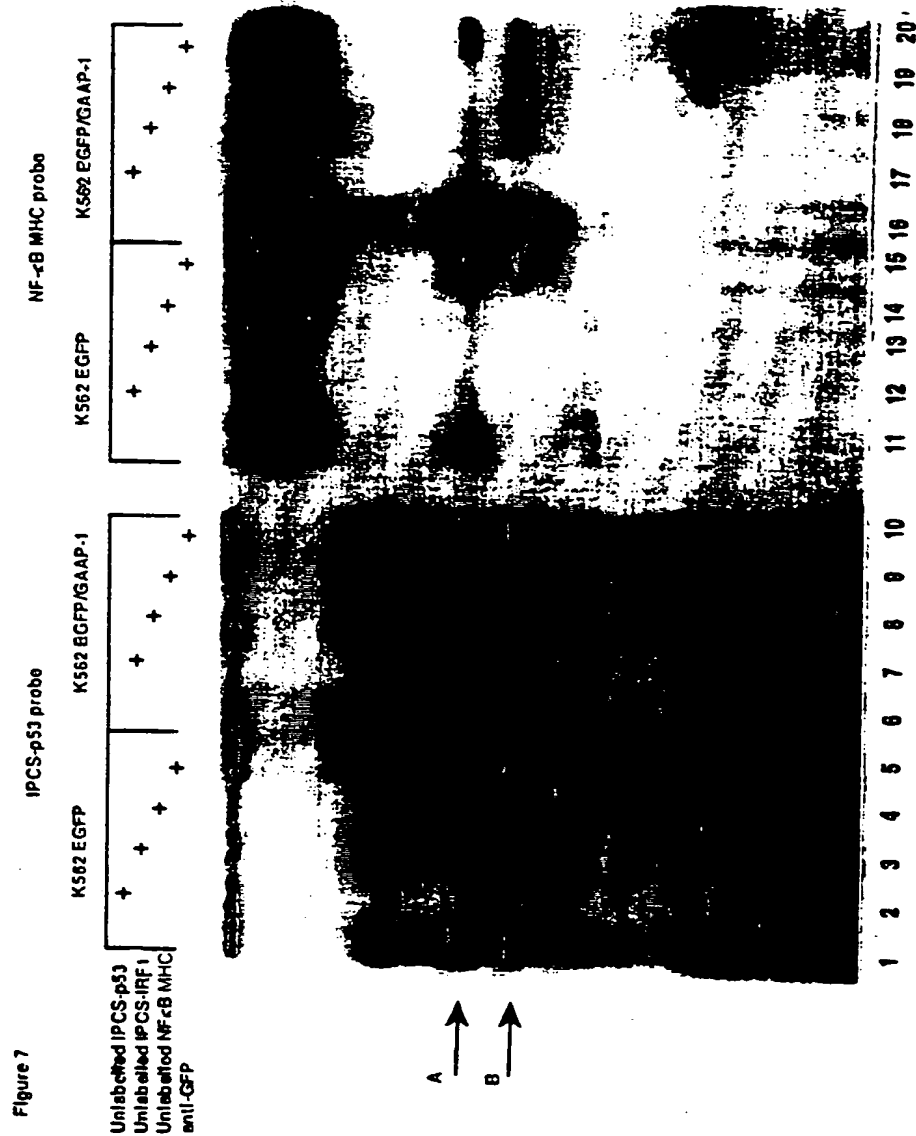


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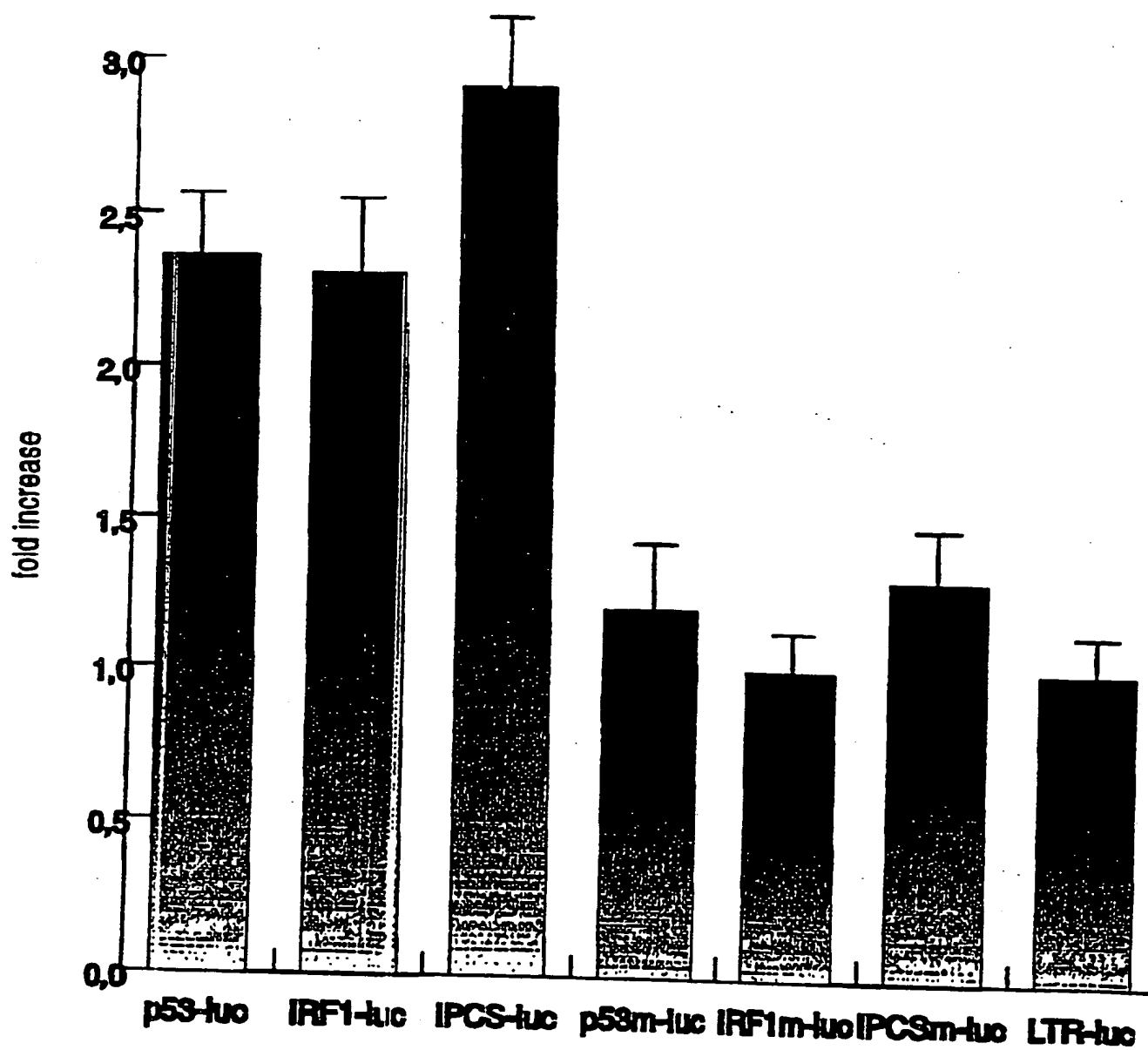
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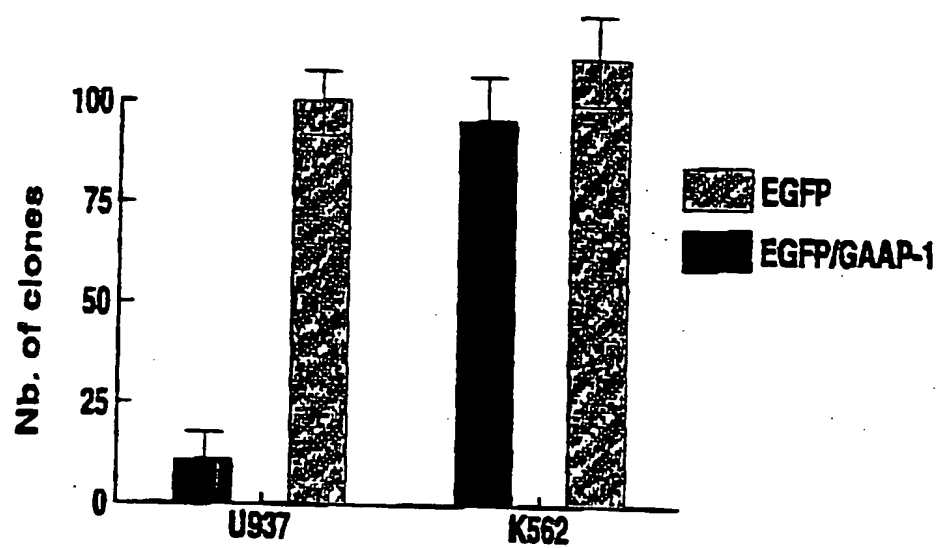
Figure 8

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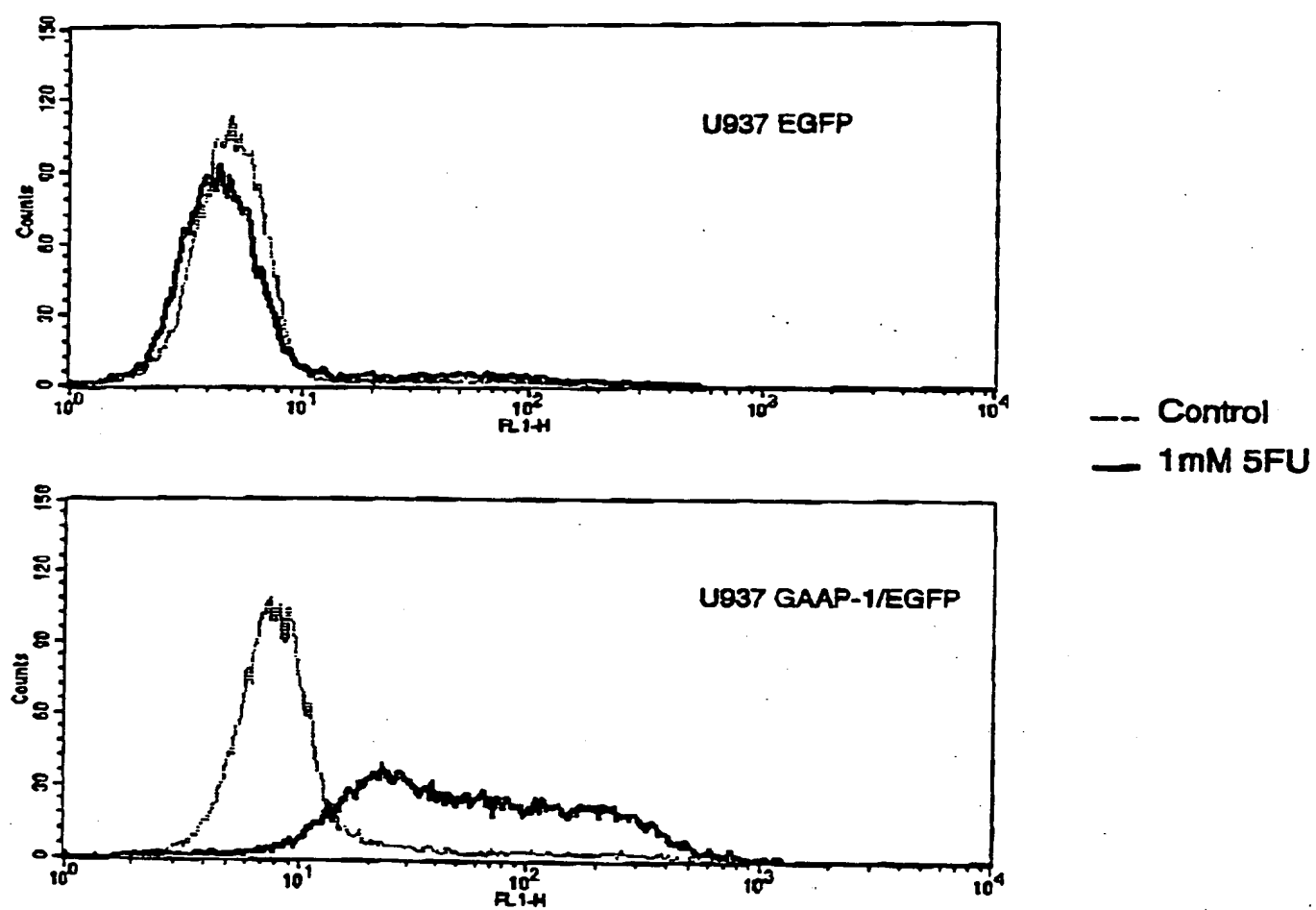
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Figure 9



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Figure 10



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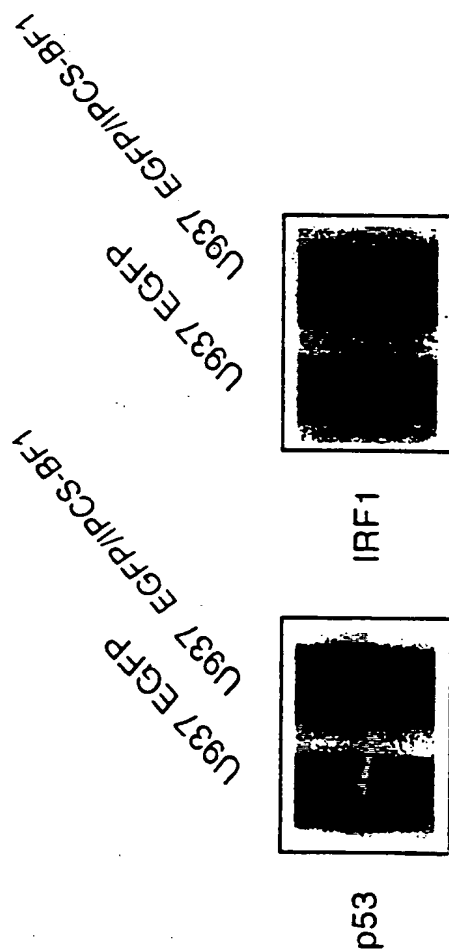
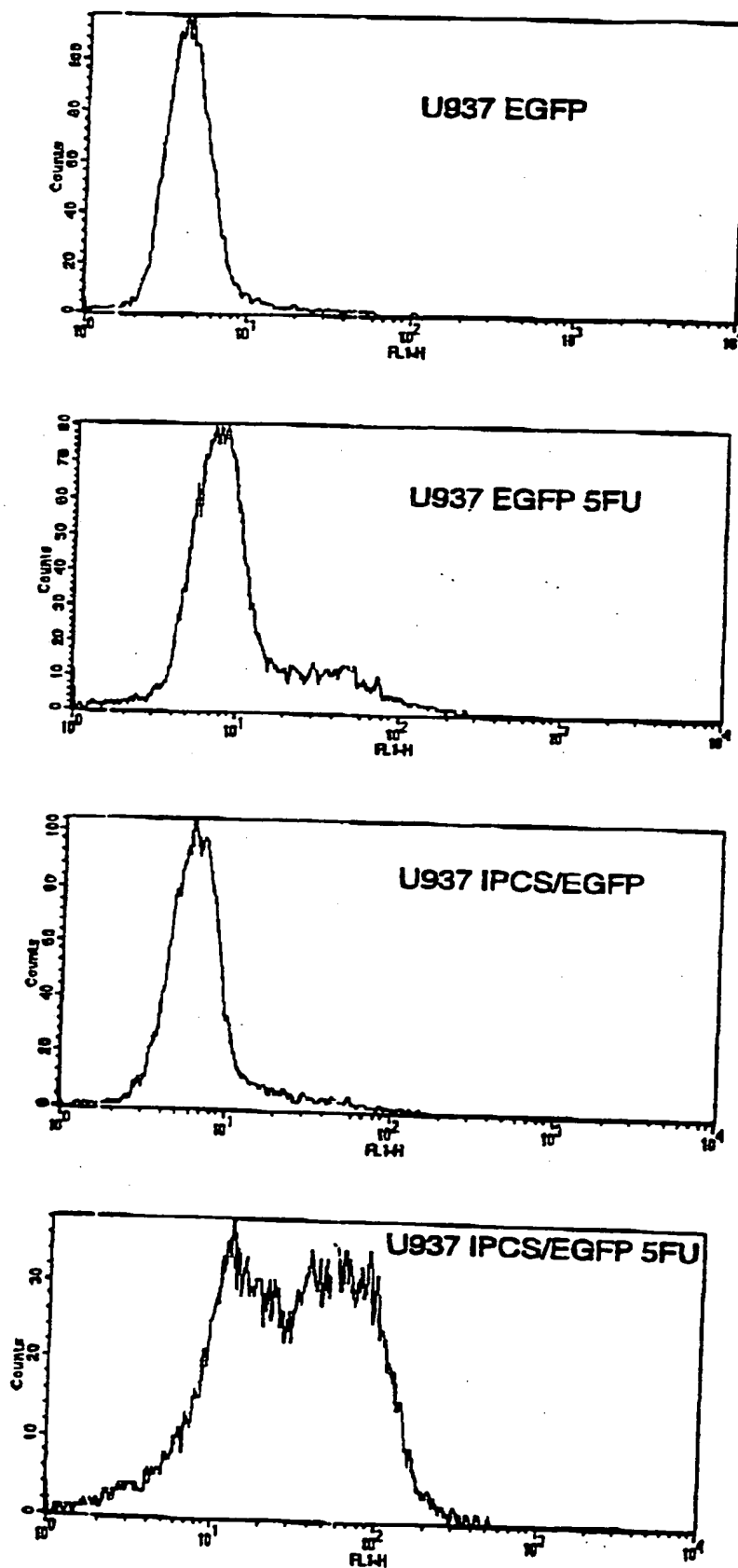


FIGURE 11

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Figure 12



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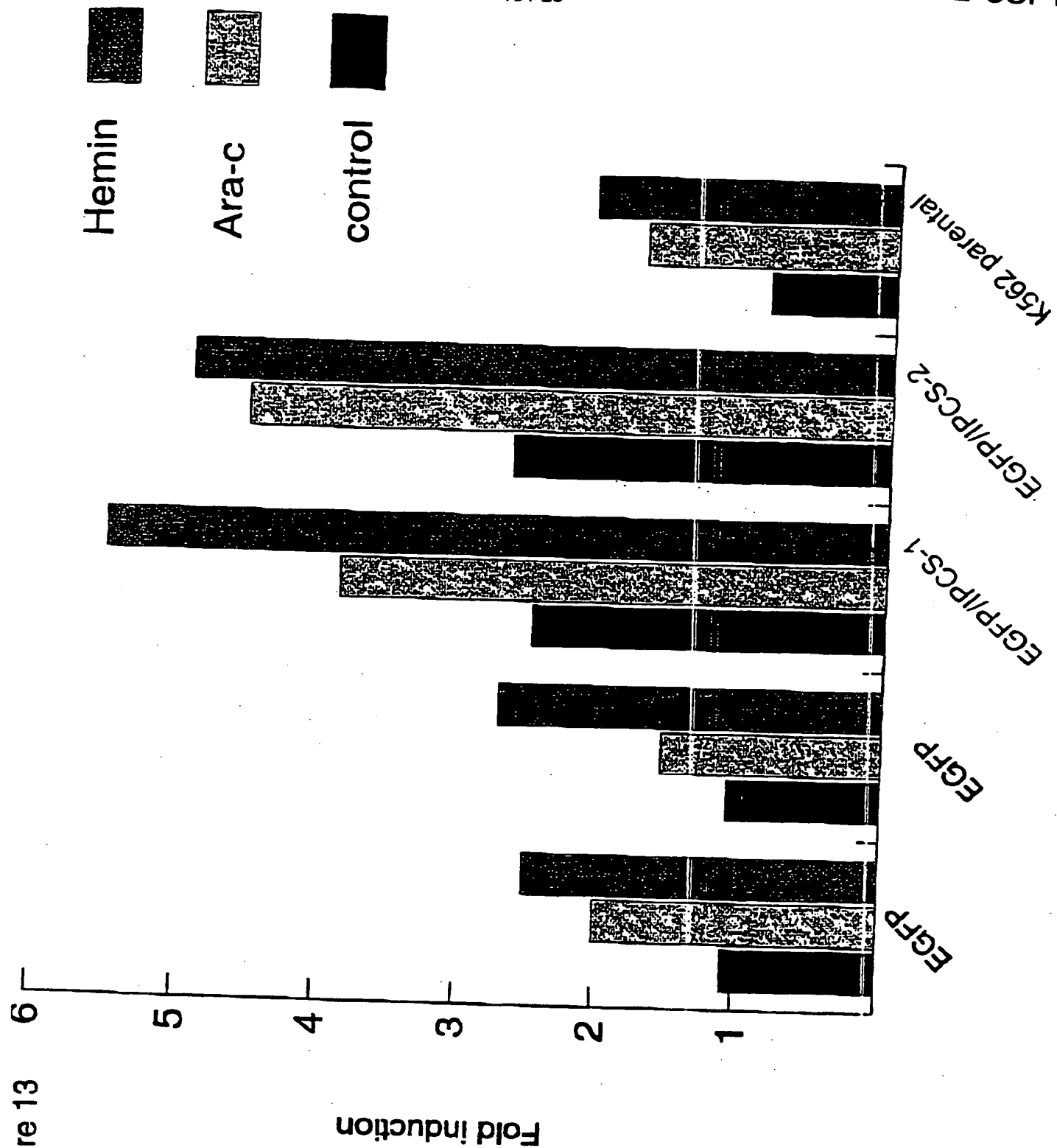


Figure 13

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1 GRP-1 CODING SEQUENCE

- Seq. No. 1

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GRP1 ATGGCATTAGGTAATCAAAAGTCCACAGTAGTTGAATTCAGCAATAAGATGCTCTGAAATTACAGTG 70
 PRDII ATGGCATTAGGTAATCAAAAGTCCACAGTAGTTGAATTCAGCAATAAGATGCTCTGAAATTACAGTG 70

GRP1 AGCAAGATAAGAAAATTCTTAAATCAAAAGTGAACCAAGAGAAATTAAATATTTGTGGGGATATA 140
 PRDII AGCAAGATAAGAAAATTCTTAAATCAAAAGTGAACCAAGAGAAATTAAATATTTGTGGGGATATA 140

GRP1 GTCAATCAAGAGTATGTATATGTCGGGAGGGAGGAGGAATACATTTGTGAAGAAATGTGGGAATA 210
 PRDII GTCAATCAAGAGTATGTATATATCCGAGGGAGGGAGAGGAATACATTTGTGAAGAAATGTGGGAATA 210

GRP1 CGTTGTAGAAACCTTAGCTGTGTAAGAAACACATACGAACCCATCAGATGTGCGGCCCTACCACTGCA 280
 PRDII CGTTGTAGAAACCTTAGCTGTGTAAGAAACACATACGAACCCATCAGATGTGCGGCCCTACCACTGCA 280

GRP1 CTTACTGTAACTTCTCTCTTAAGACTAAAGGAATCTGACAAACACATGAAGTCCAGGCCATAGCAA 350
 PRDII CTTACTGTAACTTCTCTCTTAAGACTAAAGGAATCTGACAAACACATGAAGTCCAGGCCATAGCAA 350

GRP1 GAAATGTGTGGATTATAGCCCTTCAGTAGGTTAATGATCAACAGGTACAGAGAAATCAGATGA AAA 420
 PRDII GAAATGTGTGGATTATAGCCCTTCAGTAGGTTAATGATCAACAGGTACAGAGAAATCAGATGA AAA 420

GRP1 CAGACATTCAATATAGCGGATCTGGATATGATCTTGAGAAATCTGATGGGCCAGATGAGGATCACAATG 490
 GRP1 CAGAGATTCAATATAGCGGATCTGGATATGATCTTGAGAAATCTGATGGGCCAGATGAGGATCACAATG 490

GRP1 AAATGTAGAGAGATGTGAGGACAGCCAGGCTGAATCAGTCTCTCAGCCACACCTCAGTACAGCTAG 560
 PRDII AAATGTAGAGAGATGTGAGGACAGCCAGGCTGAATCAGTCTCTCAGCCACACCTCAGTACAGCTAG 560

GRP1 CCGCAGCACTTCTCTCTAGAGTAGCTTCAGGACCTGTGAGTACTGACGAGGATGTCAAGATCAAC 630
 PRDII CCGCAGCACTTCTCTCTAGAGTAGCTTCAGGACCTGTGAGTACTGACGAGGATGTCAAGATCAAC 630

GRP1 GATTGCTTTTCTGGGGTACACAAGGACCAATGGAAGCTTCTGCCCAGGGGCTCTCTCAGCAGATGACTG 700
 PRDII GATTGCTTTTCTGGGGTACACAAGGACCAATGGAAGCTTCTGCCCAGGGGCTCTCTCAGCAGATGACTG 700

GRP1 TCTTGAGCACACACAGTCTGACTACATAGGAAGACACTCTCTCAGGGGAGGCCCAGGCAGGGTCTGTC 770
 PRDII TCTTGAGCACACACAGTCTGACTACATAGGAAGACACTCTCTCAGGGGAGGCCCAGGCAGGGTCTGTC 770

GRP1 GAGAGATGAAAACACACAMTTCCTCTCTGACACTTCCAGGTCCCGGTGTCATCAGATGCTCTGTCGAC 840

FIGURE 14A (a)

PRDII GAAGATGAAGAAGACAAATTOGGTCTGTAGACACTTCCAGGTCCCGGTGTATCAGATGTCTGTGGAC 840
 GAAP1 TACCTGAGTCAGAGAAATTCCTGAGAGTTCTATGGCTGGAAAGCTGTTCCTTATACACAGAGCCCAT 910
 PRDII TACCTGAGTCAGAGAAATTCCTGAGAGTTCTATGGCTGGAAAGCTGTTCCTTATACACAGAGCCCAT 910
 GAAP1 CATCTGTAAAGACTTCTCTCTGCTGCAAGCTGAGCAGAGCCCCAGCAGCAGCGGGGATGCTTCTGTGGC 980
 PRDII CATCTGTAAAGACTTCTCTCTGCTGCAAGCTGAGCAGAGCCCCAGCAGCAGCGGGGATGCTTCTGTGGC 980
 GAAP1 CTCACACATCTCTGACCTTCAAGAACAGAGCAGCAATTAACCTTACAGCGGACTCCAGGCTTGGCTTCT 1050
 PRDII CTCACACATCTCTGACCTTCAAGAACAGAGCAGCAATTAACCTTACAGCGGACTCCAGGCTTGGCTTCT 1050
 GAAP1 CCCCACACTCATTGTGTTTGGCACTTCTCTTTCGCTTCCAGCAGCAATGAGGACACCTTATATATGG 1120
 PRDII CCCCACACTCATTGTGTTTGGCACTTCTCTTTCGCTTCCAGCAGCAATGAGGACACCTTATATATGG 1120
 GAAP1 TTCCAGTTGGGGGATCCATGTGGTAACCTGCTGGGCTCACATACTCCAGCTTGTGTGCCCCCTCAGGCTGG 1190
 PRDII TTCCAGTTGGGGGATCCATGTGGTAACCTGCTGGGCTCACATACTCCAGCTTGTGTGCCCCCTCAGGCTGG 1190
 GAAP1 ACCAGTGCAGCTCAGCATCCCTGCTGTCAGTGTCTTTCACAGAACTTTGGGTACTCATAGGATACGGTTC 1260
 PRDII ACCAGTGCAGCTCAGCATCCCTGCTGTCAGTGTCTTTCACAGAACTTTGGGTACTCATAGGATACGGTTC 1260
 GAAP1 ACAGAGGTGTCTGGCACTACAAACCTTCTGGAGTGGCTGAATTAGCAGTGTGTGGCATGTATTCTCTA 1330
 PRDII ACAGAGGTGTCTGGCACTACAAACCTTCTGGAGTGGCTGAATTAGCAGTGTGTGGCATGTATTCTCTA 1330
 GAAP1 TGGGCCAAATCCCGGTGGCAGGCTTCAGAACTTAGTACCCAGGCTTGCAGTCACTCCCTCTGTATAG 1400
 PRDII TGGGCCAAATCCCGGTGGCAGGCTTCAGAACTTAGTACCCAGGCTTGCAGTCACTCCCTCTGTATAG 1400
 GAAP1 CATGGAAACCGTCAATATTTGTAGGCTTAGCCATACAAATATGGCCCCACAGTCCATCCAGGACTG 1470
 PRDII CATGGAAACCGTCAATATTTGTAGGCTTAGCCATACAAATATGGCCCCACAGTCCATCCAGGACTG 1470
 GAAP1 GCTCTGATGCTGTGGGACTCCAGGTTCTGACTGCAAAACCTTCTATCAGAAAGCAGCCCCCGGCTCAGG 1540
 PRDII GCTCTGATGCTGTGGGACTCCAGGTTCTGACTGCAAAACCTTCTATCAGAAAGCAGCCCCCGGCTCAGG 1540
 GAAP1 CACACATTCCAGGTTCTCCAGATCTTGACATAGCAATTGCCCCCTTAAATCCCTCAGTCAGTCAAGTAGC 1610
 PRDII CACACATTCCAGGTTCTCCAGATCTTGACATAGCAATTGCCCCCTTAAATCCCTCAGTCAGTCAAGTAGC 1610
 GAAP1 CGTGTGTCCACAGGAGCTCCGCAATGCCAGCTTCCCAAGCAAGCATGGGAGACACAAACCAAGCAG 1680

↓

FIGURE 14A (b)

PRDII CGTTGATGCACAGGGAGCTCCAGAAATGCCAGGCTTCCAAAGCAAGCATGCCGACACAAACCAAGCAG 1680

GAAP1 ACTTCTGTAGCCAGGGCAAAACCAGGTACGCGAGGACCTAGTCTCTCAGGGGTTACCTACAGTCCAGGGG 1750

PRDII ACTTCTGTAGCCAGGGCAAAACCAGGTACGCGAGGACCTAGTCTCTCAGGGGTTACCTACAGTCCAGGGG 1750

GAAP1 AAAATGCCAAAAAGTTCTGAATCCACCTGCCCCCTGCAGGTGACCATGCCAAGGCTTGATGGGCTGAGTAA 1820

PRDII AAAATGCCAAAAAGTTCTGAATCCACCTGCCCCCTGCAGGTGACCATGCCAAGGCTTGATGGGCTGAGTAA 1820

GAAP1 AATGGACACACAGAGAGGCTGGCTGGCCAAATCAGGTGAAGGCCAAGGCTGACTCACTTCCATACAGGGC 1890

PRDII AATGGACACACAGAGAGGCTGGCTGGCCAAATCAGGTGAAGGCCAAGGCTGACTCACTTCCATACAGGGC 1890

GAAP1 CAACCAGGGTCCAGGTACAAACCTCTGCTGAGGCCACATTCGAGTTTTCACAAAGGCGCTCAGGGCCAGC 1960

PRDII CAACCAGGGTCCAGGTACAAACCTCTGCTGAGGCCACATTCGAGTTTTCACAAAGGCGCTCAGGGCCAGC 1960

↓

GAAP1 AGACTCTCTCTCCAGACAGACAGGTTCCAGGGCCACAGCACTACCCGGGAGGCGAGGCGACTGTGCACCT 2030

PRDII AGACTCTCTCTCCAGACAGACAGGTTCCAGGGCCACAGCACTACCCGGGAGGCGAGGCGACTGTGCACCT 2030

GAAP1 CAGCGAAGTGAGCGAGCGATGCTGACGAGGACAGGCTTGATGATGCCAACTGATG 2084

PRDII CAGCGAAGTGAGCGAGCGATGCTGACGAGGACAGGCTTGATGATGCCAACTGATG 2084

FIGURE 14A (c)

ATGGGGCAGAAGTTTCAAAAAAAGAGA

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GCATTAGGTAATCAAAGTCCACAGTAGTTGAATTCAGCAATTAAGTTGCTCTGAAATTACAGTG

GAAP1 ACCAAGATAAAGAAATTCCTTAATCAAAGTGAACCAAGAAATTAAATTTTGTATGGAGGTATTA

GAAP1 GTCAAATCAAGAGTATGTATATGTCCGAGGCAGCCAGGGAATTAATTTGTGAAGATGTCGAATA

GAAP1 CGTTGTAAAGAAACCTACATGTTAAAGAAACACATAGCAACCCATACAGATGTCCGCCCCCAACACTGCA

GAAP1 CTACTGTACTTCTCTCTTAAAGCTAAAGGAATCTGACAAACACATGAAGTCCAGGCACATAGCAA

GAAP1 GAATGTGAGGCAATTAGGCGTCTCAGTAGGTTAATGATCAACAGGTACAGAGATCAGATGAAATA

GAAP1 CAGCAATTCAGTTATGAGCATCTGGATATGATCTTGACATCTGATGGCCAGATCAGGATCACAATG

GAAP1 AAATGTAGAGCATGATGAGGACAGCCAGGCTGAATCAGTCTCTGAGCCACCCCTAGTCACAGCTAG

GAAP1 CCGGCAGCACTTCCATCTGAGAGTAGCCTCAGCAACCTGTGAGTACTGAGAGGATGTCAAGATCAC

GAAP1 GATTGCTTTTCTGGGCTACACAGGACCCATGCTGCTCTGCCCAGGGGCTGCTCAACAGATGACTG

GAAP1 TCTGTAGCACAGGCAGTCTGACTACATAGGAGCACTCTCTCCGGGAGAGCCAGCCAGGCTGCTG

GAAP1 GACAGATGAAGACACAAATTCCTCTGTAGCACTTCCAGGTCCCGGTGTCATCAATGCTCTGTGGAC

FIGURE 14B (a)

GAAP1 TACCTGAGTCAGAGAAATTCAGAGAGTTCTATGGCAGGAAAGCTGTTCCTATAACACAGAGGCGAT

GAAP1 CATCTGTAAAGACTTCCTCTCTGCTGACGCTGAGCACAGGCGGACAGAGCGAGGGGGATGCGTTCTGTGGC

GAAP1 CTCACCATCTCTGACCGTCAAGTACAGTACGAGCAATACTCTACAGCGGACTCAGGCTTGCGTTCT

GAAP1 CCGACACTCATTTGTTTACGACCGTCTCTTTGCATTCCAGCAGCAATCGAGGACACCGTTATATATGG

GAAP1 TTCCAGTGGGGGGATCCATGTGGTAAGTCTGCTGGGCTACATACTCCAGCTTTGTGGGCGTTCAGCGCTGG

GAAP1 ACCAGTGCAGCTCAGATCCCTGCTGTCTAGTGTCTGTACAGTACTTTGGGTACTCATAGCAATACGGTC

GAAP1 ACAGAGTGTCTGGCACTACAAACCGTCTGAGTGGCTGAATTACGAGTGTGTGGCATGTATTCTTA

GAAP1 TGGGCAATCCGGGTGGCAGGCGTTCAGAACCTAAGTACCGCAGGCTTGCACTCAGTCCCGCTGTTAAG

GAAP1 CATGGAAACCGTCAATATTGTAGCGCTAGCCAAATACAAATATGGCGGACAGTCCATCCACAGGACTG

GAAP1 GCTCTGAATGCTGTGGGACTCCAGGTTCTGACTGCAACCGCTTCATCAAAAGCAGCGCGCGCGCTCAGG

GAAP1 CACACATTCCAGGTTCTCCAGTCTTTGACATAGCAATTGCGCACTTAATCCCGTCACTCAGTCAAGTAGC

GAAP1 CGTTGATCCACAGGAGCTCCGCAATGCGCAGCTTCCCAAGCAAGCATGGTAGACACAAACCAAGCAG

FIGURE 14B (b)

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PRDII CGTTCATGCACAGGGAGCTCCAGAAATGCCAGCTTCCAAAGCAAGCATGCGACATCAACCCAGCAG

GAAP1 ACTTCTGTAGCCAGGGCAAAACCAGGTACGACGGAACCGAGTCTCTCTCAGGGGTACCTACAGTCCAGGGG

GAAP1 AAAATGCAAAAAAGCTTCTGAATCCACTGCCCCCTCCAGGTGACCATGCAAGGCTTGATGGCCTGAGTAA

GAAP1 AATGGACACAGAGAGGCTGCGCTGGGCAAAATCAGGTGAGGCCCAGCCTGAACCTCACTTCCATACAGGGC

GAAP1 CAACCAGCGTCCAGTCCACAACCTCTGCTGAGGCACATTCTGAAGTTTTACAAAGCCCTCAGGCCAGC

GAAP1 AGACTCTCTCTCCAGACAGACAGGTCCCGAGGCCACAGCACTACCGGGAGGCCAGGCCACTGTGCACCT

GAAP1 CAGCGACGTGAGCAGCGATGATGAGGAGGACAGGCTTGTGATAGCAACCTGATG

FIGURE 14B (c)

GAAP-2 coding seq

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Seq No. 5

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1  ATGGGGCAGA AGTTTCAAAA AAAGAAATCT TACAGGCTGG TGTTAAAGGA
   TACCCCGTCT TCAAAGTTTT TTTCTTTAGA ATGTCCGACC ACAATTTCTT
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51  ACTTCGGAAT CCCTTAAAGA GAGCATTAGG TAATCAAAG TCCACAGTAG
   TGAAGCCTTA GGAATTTCT CTCGTAATCC ATTAGTTTTT AGGTGTCATC
-----
101 TTGAATTCAG CAATAAGAT GCCTCTGAAA TTAACAGTGA GCAAGATAAA
   AACTTAAGTC GTTATTTCTA CGGAGACTTT AATTGTCACT CGTTCATTT
-----
151 GAAAATTCCT TAATCAAAG TGAACCAAGA AGAATTAAJA TATTTGATGG
   CTTTTAAGGA ATTAGTTTTT ACTTGGTTCT TCTTAATTTT ATAAACTACC
-----
201 AGGATATAAG TCAATGAAG AGTATGTATA TATCCGAGGC AGGGGAAGAG
   TCCTATATTC AGTTTACTTC TCATACATAT ATAGGCTCCG TCCCTTCTC
-----
251 GAAAATACAT TTGTGAAGAA TGTGGAATAC GTTGTAAAGAA ACCTAGCATG
   CTTTATGTA AACACTTCTT ACACCTTATG CAACATTCTT TGGATCGTAC
-----
301 TTAAGAAAC ACATACGAAC CCATACAGAT GTCCGCCCTT ACCACTGCAC
   AATTTCTTTG TGTATGCTTG GGTATGTCTA CAGGCGGGGA TGGTGACGTG
-----
351 TTAAGTAAAC TTCTCCTTTA AGACTAAAGG AAATCTGACA AAACACATGA
   AATGACATTG AAGAGGAAAT TCTGATTTCC TTTAGACTGT TTTGTGTACT
-----
401 AGTCCAAGGC ACATAGCAAG AAATGTGTGG ATTTAGGCAT CTCAGTAGGT
   TCAGGTTCCG TGTATCGTTC TTTACACACC TAAATCCGTA GAGTCATCCA
-----
451 TTAATAGATG AACAGGATAC AGAAGAATCA GATGAAAAAC AGAGATTGAG
   AATTATCTAC TTGTCTATG TCTTCTTAGT CTACTTTTIG TCTCTAAGTC
-----
501 TTATGAGCGA TCTGGATATG ATCTTGAAGA ATCTGATGCC CCAGATGAGG
   AATACTCGCT AGACCTATAC TAGAATTCT TAGACTACCG GGTCTACTCC
-----
551 ATGACAATGA AAATGAAGAC GATGATGAGG ACAGCCAGGC TGAATCAGTC
   TACTGTTACT TTTACTTCTG CTACTACTCC TGTGCGTCCG ACTTAGTCAG
-----
601 CTGTCAGCCA CACCCTCAGT CACAGCTAGC CCGCAGCACC TTCCATCTAG
   GACAGTCGGT GTGGGAGTCA GTGTCGATCG GGCCTCGTGG AAGGTAGATC
-----
651 AAGTAGCCTT CAGGACCTTG TGAGTACTGA CGAGGATGTC AGGATCACCG
   TTCATCGGAA GTCCTGGGAC ACTCATGACT GCTCCTACAG TCCTAGTGCC
-----
701 ATTGCTTTTC TGGGGTACAC ACGGACCCAA TGGACGTTCT GCCCAGGGCG
   TAACGAAAG ACCCATGTG TGCTTGGGT ACCTGCAAGA CGGGTCCCGC
-----
751 CTGCTCACCA GAATGACTGT CCTGAGCACA GCACAGTCTG ACTACAATAG
   GACGAGTGGT CTTACTGACA GGACTCGTGT CGTGTGAGC TGATGTTATC
-----
801 GAAGACACTC TCTCCGGGGA AGGCCAGGCA GCGTGCTGCT AGAGATGAAA
   CTTCTGTGAG AGAGGCCCCCT TCCGGTCCGT CGCAGGACGCT TCTTACTTT
-----
851 ACGACACAAT TCCGTCTGTA GACACTTCCA GGTCCCCGTG TCATCAGATG
   TGCTGTGTTA AGGCAGACAT CTGTGAAGGT CCAGGGGCA AGTAGTCTAC
-----
901 TCTGTGGACT ACCCTGAGTC AGAAGAAATT CTGAGAAGTT CTATGGCAGG
   AGACACCTGA TGGGACTCAG TCTTCTTTAA GACTTTCA GATACCGTCC
-----

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FIGURE 14C (a)

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951  AAAAGCTGTT GCTATAACAC AGAGCCCATC ATCTGTAAGA CTCCTCCTG
      TTTTCGACAA CGATATTGTG TCTCGGGTAG TAGACATTCT GAAGGAGGAC
-----
1001  CTGCAGCTGA GCACAGCCCC CAGACAGCAG CGGGGATGCC TTCTGTGGCC
      GACCTCGACT CGTGTCTGGG GTCTGTCTGT GCCCTTACCG AAGACACCGG
-----
1051  TCACCACATC CTGACCCTCA AGAACAGAAG CAGCAAATTA CTCTACAGCC
      AGTGGTGTAG GACTGGGAGT TCTTGTCTTC GTCGTTTATT GAGATGTCGG
-----
1101  GACTCCAGGC TTGCCTTCTC CCCACACTCA TTTGTTTAGC CACCTTCCTT
      CTGAGGTCCG AACGGAAGAG GGGTGTGAGT AAACAAATCG GTGGAAGGAA
-----
1151  TGCATTCCCA GCAGCAATCG AGGACACCTT ATAATATGCT TCCAGTTGGG
      ACGTAAGGGT CGTCGTTAGC TCCTGTGGAA TATTATACCA AGGTCAACCC
-----
1201  GGGATCCATG TGGTACCTGC TGGCCTCACA TACTCCACCT TTGTGCCCT
      CCCTAGGTAC ACCATGGACG ACCGGAGTGT ATGAGGTGCA AACACGGGGA
-----
1251  TCAGGCTGGA CCAGTGCAGC TCACGATCCC TGCTGTCAGT GTCGTTTACA
      AGTCCGACCT GGTACAGTCG AGTGCTAGGG ACGACAGTCA CAGCAAGTGT
-----
1301  GAACCTTGGG TACTCATAGG AATACGGTCA CAGAAGTGTG TGGCACTACA
      CTTGAAACCC ATGAGTATCC TTATGCCAGT GTCTTCACAG ACCGTGATGT
-----
1351  AACCCTGCTG GAGTGGCTGA ATTAAGCAGT GTTGTGCCAT GTATTCTAT
      TTGGGACGAC CTCACCGACT TAATTCGTCA CAACACGGTA CATAAGGATA
-----
1401  CGGCCAAATC CGCGTGCCAG GCCTTCAGAA CCTAAGTACT CCAGGCTTGC
      GCCGGTTTAG GCGCACGGTC CGGAAGTCTT GGATTTCATG GGTCCGAACG
-----
1451  AGTCACTCCC CTCGTTAAGC ATGGAAACCG TCAATATTGT AGGCCTAGCC
      TCAGTGAGGG GAGCAATTCT TACCTTTGGC AGTTATAACA TCCGGATCGG
-----
1501  AATACAAATA TGGCCCCACA AGTCCATCCA CCAGGACTGG CTCTGAATGC
      TTATGTTTAT ACCGGGGTGT TCAGGTAGGT GGTCTGTAGC GAGACTTACG
-----
1551  TGTCGGACTG CAGGTTCTGA CTGCAAACCC TTCATCACA AGCAGCCCCG
      ACAGCCTGAC GTCCAAGACT GACGTTTGGG AACTAGTGTG TCGTCGGGGC
-----
1601  CCCCTCAGGC ACACATTCCA GGTCTCCAGA TCTTGAACA AGCATTGCCC
      GGGGAGTCCG TGTGTAAGGT CCAGAGGTCT AGAACTTGTA TCGTAACGGG
-----
1651  ACCTTAATCC CCTCAGTCAG TCAAGTAGCC GTTGATGCAC AGGGAGCTCC
      TGGAAATTAGG GGAGTCAGTC AGTTCATCGG CAACTACGTG TCCCTCGAGG
-----
1701  AGAAATGCCA GCTTCCCAA GCAAAGCATG CGAGACACA CCCAAGCAGA
      TCTTTACGGT CGAAGGGTTT CGTTTCGTAC GCTCTGTGTT GGGTTCTGTT
-----
1751  CTTCTGTAGC CAGCGCAAAC CAGGTCAGCA GGACCGAGTC TCCTCAGGGG
      GAAGACATCG GTCGCGTTTG GTCCAGTCGT CCTGGCTCAG AGGAGTCCCC
-----
1801  TTACCTACAG TCCAGCGGGA AAATGCAAAA AAAGTTCTGA ATCCACCTGC
      AATGGAATGC AGGTGCGCCCT TTTACGTTTT TTTCAAGAC TAGGTGGACC
-----
1851  CCTGTCAGGT GACCATGCAA GGCTTGATGG CCTGAGTAA ATGGACACAG
      GGGACGTCCA CTGGTACGTT CCGAACTACC GGACTCATT TACCTGTGTC
-----

```

FIGURE 14C (b)

1901 AGAAGGCTGC CTCGGCAAAT CACGTGAAGC CCAAGCCTGA ACTCACTTCC
TCTTCCGACG GAGCCGTTTA GTGCACITCG GGTTCGGACT TGAGTGAAGG

1951 ATACAGGGCC AACCAGCGTC CACGTCACAA CCTCTGCTGA AGGCACATTC
TATGTCCCGG TTGGTCGCAG GTGCAGTGTT GGAGACGACT TCCGTGTAAG

2001 TGAAGTTTTT ACAAAGCCCT CAGGCCAGCA GACTCTCTCT CCAGACAGAC
ACTTCAAAAA TGTTTCGGGA GTCCGGTCGT CTGAGAGAGA GGTCTGTCTG

2051 AGGTTCCCAG GCCCAGAGGA CTACCGCGGA GGCAGCCCAC TGTGCACTTC
TCCAAGGGTC CGGGTGTCTT GATGGCGCCT CCGTCGGGTG ACACGTGAAG

2101 AGCGACGTGA GCAGCGATGA TGACGAGGAC AGGCTTGTGA TAGCAACCTG
TCGCTGCACT CGTCGCTACT ACTGCTCCTG TCCGAACAAT ATCGTTGGAC

2151 A
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FIGURE 14C (c)

2 GAAP-1 POLYPEPTIDE

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xGAAP-1

GAAP1	MALGNQKSTWVEFSNKAASEINSEQDRENSLRSEPRKIDFDGGYKSESVYVVRGGGGKYTCRECGI	70
PRDII	MALGNQKSTWVEFSNKAASEINSEQDRENSLRSEPRKIDFDGGYKSESVYVVRGGGGKYTCRECGI	70
GAAP1	RCKGPSMLKKHIRHIDVRPYHCTYCNFSPTKRGMLTKHMSKAHKKKCVILGVSUGLIDEDQDTRSDER	140
PRDII	RCKGPSMLKKHIRHIDVRPYHCTYCNFSPTKRGMLTKHMSKAHKKKCVILGVSUGLIDEDQDTRSDER	140
GAAP1	QRFPSYERSGYDLSESDDGPDIDNEVEDDEDSDQAESVLATPSVDTASPOHLPSRSSLDQFVSTDEDVRTT	210
PRDII	QRFPSYERSGYDLSESDDGPDIDNEVEDDEDSDQAESVLATPSVDTASPOHLPSRSSLDQFVSTDEDVRTT	210
GAAP1	DCFSGVHTDPMVLPRALLTRMTVLSTAQSDYNRKTLSPGARQRAARDENDITPSVDTSRSPCHQMSVD	280
PRDII	DCFSGVHTDPMVLPRALLTRMTVLSTAQSDYNRKTLSPGARQRAARDENDITPSVDTSRSPCHQMSVD	280
GAAP1	YFSEETLRSSMAGKAVATTQSPSSVRLPFAAAHSPQTAAGMPSVASPHFDQEQKQQTILQPTFGLPS	350
PRDII	YFSEETLRSSMAGKAVATTQSPSSVRLPFAAAHSPQTAAGMPSVASPHFDQEQKQQTILQPTFGLPS	350
GAAP1	PETHLFSHLPILHSQQQSETPYAMVPVGGIHWVPAGLITYSTFVPLQAGFVQLITPAVSWVERTLGTHRTIV	420
PRDII	PETHLFSHLPILHSQQQSETPYAMVPVGGIHWVPAGLITYSTFVPLQAGFVQLITPAVSWVERTLGTHRTIV	420
GAAP1	TEVSGTINEAGVAELSSWFCEIPGQIRVPGQLNLSTFGLOSLEPSLSMETATVGLANDMAFQVHPFGL	490
PRDII	TEVSGTINEAGVAELSSWFCEIPGQIRVPGQLNLSTFGLOSLEPSLSMETATVGLANDMAFQVHPFGL	490
GAAP1	ALNAVGLQVLITANPSSQSSPAPQAHIPGLQILNIALPTILPSVSQVAVDQCAPMEASQSKACETQPRQ	560
PRDII	ALNAVGLQVLITANPSSQSSPAPQAHIPGLQILNIALPTILPSVSQVAVDQCAPMEASQSKACETQPRQ	560
GAAP1	TSVASANQVSRITESPQGLPTVQRENARKVLNPPAPAGDHARLDGLSRMDTERAASANEVKTPELITSIQG	630
PRDII	TSVASANQVSRITESPQGLPTVQRENARKVLNPPAPAGDHARLDGLSRMDTERAASANEVKTPELITSIQG	630
GAAP1	QFASTSQPLIKAHSEVFTKPSGQQTILSPDRQVFRPTDLERRQPTVHPSDVSSDDDEDRWTAT	694
PRDII	QFASTSQPLIKAHSEVFTKPSGQQTILSPDRQVFRPTDLERRQPTVHPSDVSSDDDEDRWTAT	694

FIGURE 15 A

2 GAAP-1 POLYPEPTIDE

Seq No 4

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>GAAP-1

M GQKFQKKR . ALGQKSTWVEFSNRDASEINS EDDKENS LIRSEPRRIKIPDGYSNEEVVYVRGSGGKYICEBOGI

GAAP1 RCKQPSMLRKHIRKHTOVRPYHCTYCNFSPTKGNLTRHMRSGHRSKRVILGVSUGLIDSQOTEESEDEK

GAAP1 QRFYSYERSGYDLSESQGFDEDDNENEDDDSDQAESVLSATPSVTASPOHLPSRSSLODPVSTDEOVRTT

GAAP1 DCFSGVEIDEMOVLPRALLTRMTVLSTAQSDYNRRILSPGRARQRAARDENDITFSVDTSRSPCHQMSVD

GAAP1 YPESSEILRSSMAGKAVAITQSPSSVRLPFAAAEHSPTAGNPSVASHPDPQEQEQOITLOFTPLPS

GAAP1 PHIRLFSHLP LHSQQSPTFYNMVPVGGIRWVPAGLTYSTFVLOAGPVQITFAVSVVHRTLCIHRNTV

GAAP1 TEVSGTINPAGVAELSSWPCIPITGQIRVPGLQNLSTFGLQSLPSLSMEIVNIVGLANTMAPQVHPFGL

GAAP1 A LNAVGLQULTANPSSQSSPAPQAHIFGLQILNIALFILIPSVSQVAVDAGAPEMPASQSKACETQPRQ

GAAP1 TSVASANQVERTESQGLPTVQRENARKVLNPPAPAGCHARLDGLSKMDEKAASANEVKKPELTSIQG

GAAP1 QPASTSQPLLKAHSEVFTGSGQQLSPDRQVPRPTALPRQPTVHFSQVSSQDDDEDLVIAT

FIGURE 15 B

GAAP-2 - Seq No. 6.

1 MGQKFQKKKS YRLVLKELRN PLKRALGNQK STVVEFSNKO ASEINSEQDK

51 ENSLIKSEPR RIKIFDGGYK SNEEYVYIRG RGRGKYICEE CGIRCKKPSM

101 LKKHIRTHTD VRPYHCTYCN FSFKTKGNLT KFMKSKAHSK KCVDLGISVG

151 LIDEQDTEES DEKQRFYSYER SGYDLEESDG PDEDDNENDO DDEDSQAESV

201 LSATPSVTAS PQHLPSRSSL QDPVSTDEDV RITDCTSGVH TDFMDVLPRA

251 LLTRMTVLST AQSDYNRCTL SPGKARQRAA RDENDTIPSV DTSRSPCHQM

301 SVDYPESEEI LRSSMAGKAV AITQSPSSVR LPPAAAEHSP QTAAGMPSVA

351 SPHPDPQEQK QQITLQPTPG LPSPHTHLFS HLPPLHSQQQS RTPYNMVPVG

401 GIHVVPAGLT YSTFVPLQAG PVQLTIPAVS VVHRTLGTNR NTVTEVSGTT

451 NPAGVAELSS VVPCIPIGQI RVPGLQNLST PGLQSLPSLS METVNIVGLA

501 NTNMAPOVHP PGLALNAVGL QVLTANPSSQ SSPAPQAHIP GLQILNIALP

551 TLIPSVSQVA VDAQGAPEMP ASQSKACETQ PKQTSVASAN QVSRTEPQG

601 LPTVQRENAK KVLNPPAPAG DHARLDGLSK MDTEKAASAN HVKPKPELTS

651 IQGQPASTSQ PLLKAHSEVF TKPSGQOTLS PDRQVPRPTG LPRRQPTVHF

701 SDVSSDDDED RLVIAT

FIGURE 15 C

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Figure 16

